

NCBI Blast:seq id no:3 vs. McCaffrey no.1

Page 1 of 3

**BLAST Basic Local Alignment Search Tool**[Edit and Resubmit](#) [Save](#) [Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

**seq id no:3 vs. McCaffrey no.1**Results for:  lcl|55517 None(206bp) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|55517

lcl|55517

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

55519

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ Citation

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, click here

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#)**Search Parameters**

Program	blastn
Word size	7
Expect value	10
Hlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 3582

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

**BLAST Basic Local Alignment Search Tool**

• Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

**seq id no:3 vs. McCaffrey no.2**

Results for:  lcl|28559 None(206bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|28559

lcl|28559

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

28561

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

---

**Search Parameters**

Program blastn  
Word size 7  
Expect value 10  
Hitlist size 100  
Match/Mismatch scores 2,-3  
Gapcosts 5,2  
Low Complexity Filter Yes  
Filter string L,m;  
Genetic Code 1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 3582

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

**BLAST Basic Local Alignment Search Tool**

EXHIBIT \*

[Edit](#) and [Resubmit](#) [Save](#) [Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

**seq id no:3 vs. McCaffrey no 3**Results for:  [cl|61181 None(206bp)]

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

[cl|61181

cl|61181

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

61183

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**BLASTN 2.2.22+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#)

**Search Parameters**

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

**Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

## Results Statistics

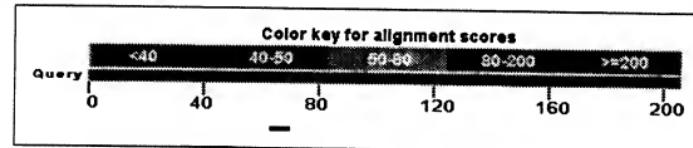
Effective search space 3582

### Graphic Summary

### Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Dot Matrix View**Plot of Icl|61181 vs 61183 [?]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

**Sequences producing significant alignments:**  
(Click headers to sort columns)

---

61183

13.9 13.9 3% 0.23 100%

Alignments Select All Get selected sequences Distance tree of results Multiple alignment 

>lcl|61183  
Length=25  
Score = 13.9 bits (14), Expect = 0.23  
Identities = 7/7 (100%), Gaps = 0/7 (0%)  
Strand=Plus/Plus  
Query 65 GCCTAAGT 71  
Sbjct 18 GCCTAAGT 24

Select All Get selected sequences Distance tree of results Multiple alignment 

**BLAST Basic Local Alignment Search Tool**

• Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

**seq id no:3 vs. McCaffrey no 4**

Results for: "Icl|4723 None(206bp)"

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

Icl|4723  
Icl|4723

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

4725

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

**Search Parameters**

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 3582

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

**BLAST Basic Local Alignment Search Tool**

• Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

**seq id no:3 vs. McCaffrey no 4**

Results for  lcl|4723 None(206bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|4723

lcl|4723

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

4725

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ Citation

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, click here

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

---

**Search Parameters**

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 3582

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

## BLAST Basic Local Alignment Search Tool

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

### seq id no:3 vs. McCaffrey no 5

Results for:  lcl|21471 None(206bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|21471  
lcl|21471

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

21473

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search](#) [Summary](#) [\[Taxonomy reports\]](#)

## Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 3582

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

**BLAST Basic Local Alignment Search Tool**[Edit](#) and [Resubmit](#) [Save](#) [Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

**seq id no:3 vs. McCaffrey no 6**Results for:  31433 None(206bp) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID** lcl|31433  
 lcl|31433**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

31435

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**BLASTN 2.2.22+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

**Search Parameters**

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

**Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

## Results Statistics

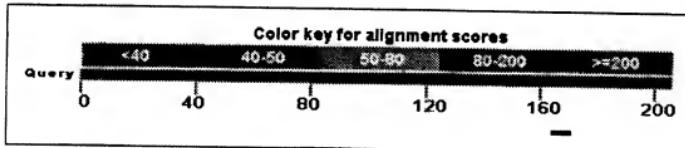
Effective search space 3582

### Graphic Summary

#### Distribution of 1 Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[Dot Matrix View](#)

### Plot of Icl|31433 vs 31435 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:  
(Click headers to sort columns)

31435	13.9	13.9	3%	0.23	100%
-------	------	------	----	------	------

Alignments Select All Get selected sequences Distance tree of results Multiple alignment [Help](#)

>lc1|31435  
Length=25

Score = 13.9 bits (14), Expect = 0.23  
Identities = 7/7 (100%), Gaps = 0/7 (0%)  
Strand=Plus/Plus

Query 166 GAACTCC 172  
Sbjct 11 ||||||| GAACTCC 17

Select All Get selected sequences Distance tree of results Multiple alignment [Help](#)

**BLAST Basic Local Alignment Search Tool**

EXHIBIT 1

[Edit](#) and [Resubmit](#) [Save](#) [Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

**seq id no:3 vs. McCaffrey no 7**Results for:  [cl|38455 None(206bp)]

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**[cl|38455  
cl|38455**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

38457

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**BLASTN 2.2.22+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]**Search Parameters**

Program blastn  
Word size 7  
Expect value 10  
Hitlist size 100  
Match/Mismatch scores 2,-3  
Gapcosts 5,2  
Low Complexity Filter Yes  
Filter string L,m;  
Genetic Code 1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408148	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 3582

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

## BLAST Basic Local Alignment Search Tool

• Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

### SEQ ID NO. 10 vs. McCAFFREY NO.1

Results for:  Icl|45183 None(71bp) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

Icl|45183  
Icl|45183

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

71

**Subject ID**

45185

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ Citation

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search](#) [Summary](#) [\[Taxonomy reports\]](#)

### Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408148	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 1320

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

**BLAST Basic Local Alignment Search Tool**

• Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

**SEQ ID NO. 10 vs. McCAFFREY NO.2**

Results for:  lcl|53051 None(71bp) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|53051  
lcl|53051

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

71

**Subject ID**

53053

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jingui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

**Search Parameters**

Program blastn  
Word size 7  
Expect value 10  
Hitlist size 100  
Match/Mismatch scores 2,-3  
Gapcosts 5,2  
Low Complexity Filter Yes  
Filter string L,m;  
Genetic Code 1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 1320

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

**BLAST Basic Local Alignment Search Tool**

•  
[Edit and Resubmit](#) [Save Search](#) [Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

**SEQ ID NO. 10 vs. McCAFFREY NO.3**

Results for:  [cl|3921 None(71bp)]

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

[cl|3921  
[cl|3921

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

71

**Subject ID**

3923

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, click here

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#)

**Search Parameters**

Program                   blastn  
Word size                7  
Expect value             10  
Hitlist size             100  
Match/Mismatch scores 2,-3  
Gapcosts                5.2  
Low Complexity Filter Yes  
Filter string           L,m;  
Genetic Code            1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 1320

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence

[?]

---

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

**BLAST Basic Local Alignment Search Tool**

• Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

**SEQ ID NO. 10 vs. McCAFFREY NO.4**

Results for:  [cl|59547 None(71bp)]

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

[cl|59547  
cl|59547]

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

71

**Subject ID**

59549

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ Citation

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, click here

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

**Search Parameters**

Program blastn  
Word size 7  
Expect value 10  
Hitlist size 100  
Match/Mismatch scores 2,-3  
Gapcosts 5,2  
Low Complexity Filter Yes  
Filter string L,m;  
Genetic Code 1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 1320

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

## BLAST Basic Local Alignment Search Tool

• Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

### SEQ ID NO. 10 vs. McCAFFREY NO.5

Results for: [1cl10651 None(71bp)]

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

1cl10651  
1cl10651

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

71

**Subject ID**

10653

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

## Search Parameters

Program blastn  
Word size 7  
Expect value 10  
Hitlist size 100  
Match/Mismatch scores 2,-3  
Gapcosts 5,2  
Low Complexity Filter Yes  
Filter string L,m;  
Genetic Code 1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408148	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 1320

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

**BLAST Basic Local Alignment Search Tool**

• Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

**SEQ ID NO. 10 vs. McCAFFREY NO.6**

Results for:  [cl|26449 None(71bp)]

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

cl|26449  
cl|26449

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

71

**Subject ID**

26451

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ Citation

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, click here

Other reports: Search Summary [Taxonomy reports]

**Search Parameters**

Program blastn  
Word size 7  
Expect value 10  
Hitlist size 100  
Match/Mismatch scores 2,-3  
Gapcosts 5,2  
Low Complexity Filter Yes  
Filter string L;m;  
Genetic Code 1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408148	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 1320

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

**BLAST Basic Local Alignment Search Tool**

• Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

**SEQ ID NO. 10 vs. McCAFFREY NO.7**

Results for: \*lcl|32359 None(71bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|32359

lcl|32359

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

71

**Subject ID**

32361

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

**Search Parameters**

Program blast  
Word size 7  
Expect value 10  
Hitlist size 100  
Match/Mismatch scores 2,-3  
Gapcosts 5,2  
Low Complexity Filter Yes  
Filter string L,m;  
Genetic Code 1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### Results Statistics

Effective search space 1320

[Graphic Summary](#)

### Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.